

SEQUENCE LISTING

<110> Mahajan, Pramod B.

<120> Rad2/FEN-1 Orthologues and Uses
Thereof

<130> 0961D

<150> 09/426,557

<151> 1999-10-22

<150> 60/112,332

<151> 1998-12-15

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<170> FastSEQ for Windows Version 3.0

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<222> (85)...(1221)

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                  1                    5

ctg gcg gac aat gcg ccc aag gcg atg aag gag cag aag ttc gag agc      159
Leu Ala Asp Asn Ala Pro Lys Ala Met Lys Glu Gln Lys Phe Glu Ser
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tac ttc gcc cgc aaa atc gcc gtc gac gcc agc atg agc ata tac cag      207
Tyr Phe Gly Arg Lys Ile Ala Val Asp Ala Ser Met Ser Ile Tyr Gln
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ttc ctg att gta gtt gga agg aca gcc atg gaa act ctc aca aat gaa      255
Phe Leu Ile Val Val Gly Arg Thr Gly Met Glu Thr Leu Thr Asn Glu
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gct ggt gaa gtc act agt cat ttg caa gga atg ttc aac cgg aca ata      303
Ala Gly Glu Val Thr Ser His Leu Gln Gly Met Phe Asn Arg Thr Ile
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aga tta ctg gaa gcg gga atc aag cca gtt tat gtt ttt gat gcc aag      351
Arg Leu Leu Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp Gly Lys
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cct cct gat atg aag aaa caa gag ctt gct aaa aga tac tca aaa aga      399
Pro Pro Asp Met Lys Lys Gln Glu Leu Ala Lys Arg Tyr Ser Lys Arg
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gat gat gca acc aaa gat ctg act gag gca gta gag gta gga gat aaa      447
Asp Asp Ala Thr Lys Asp Leu Thr Glu Ala Val Glu Val Gly Asp Lys

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cac aac gaa gat tgt aaa cgg cta tta aga ctt atg ggg gtt cct gtt His Asn Glu Asp Cys Lys Arg Leu Leu Arg Leu Met Gly Val Pro Val 140 145 150	543
gta gag gca cct tct gaa gca gaa gca gaa tgt gca gcc ctt tgc ata Val Glu Ala Pro Ser Glu Ala Glu Ala Glu Cys Ala Ala Leu Cys Ile 155 160 165	591
aac gat aag gtg ttc gct gtt gct tca gaa gat atg gac tcc ctt act Asn Asp Lys Val Phe Ala Val Ala Ser Glu Asp Met Asp Ser Leu Thr 170 175 180 185	639
ttt ggg gct cca cgg ttc ctt cgt cat tta atg gat cca agt tcc aag Phe Gly Ala Pro Arg Phe Leu Arg His Leu Met Asp Pro Ser Ser Lys 190 195 200	687
aaa ata cct gtg atg gaa ttt gat gtt gcc aag gtt ttg gag gag ctt Lys Ile Pro Val Met Glu Phe Asp Val Ala Lys Val Leu Glu Glu Leu 205 210 215	735
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gac tat tgt gat agc atc aaa ggt atc ggg ggg caa aca gct ctg aaa Asp Tyr Cys Asp Ser Ile Lys Gly Ile Gly Gln Thr Ala Leu Lys 235 240 245	831
ctt att cgt caa cat ggg tcc ata gaa agc atc ttg gag aat ctt aat Leu Ile Arg Gln His Gly Ser Ile Glu Ser Ile Leu Glu Asn Leu Asn 250 255 260 265	879
aaa gac aga tat caa att cct gag gac tgg cct tac caa gaa gct cga Lys Asp Arg Tyr Gln Ile Pro Glu Asp Trp Pro Tyr Gln Glu Ala Arg 270 275 280	927
cgc ttg ttc aag gag cct aat gtc aca ttg gat att cct gag cta aaa Arg Leu Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro Glu Leu Lys 285 290 295	975
tgg act gca cct gat gag gag ggt ctc ata agt ttc ctg gta aaa gat Trp Thr Ala Pro Asp Glu Glu Gly Leu Ile Ser Phe Leu Val Lys Asp 300 305 310	1023
aat ggt ttc aac gaa gat cgg gtg aca aag gcc ata gag aag atc aaa Asn Gly Phe Asn Glu Asp Arg Val Thr Lys Ala Ile Glu Lys Ile Lys 315 320 325	1071
tct gcc aag aat aaa tcg tcg caa gga aga ctc gag tcc ttt ttc aag Ser Ala Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser Phe Phe Lys 330 335 340 345	1119
cca act gcc acc aca tca gca cgg cta aaa cgg aag gag act tcg gat Pro Thr Ala Thr Ser Ala Pro Leu Lys Arg Lys Glu Thr Ser Asp 350 355 360	1167

Val Thr Lys Ala Ile Glu Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser
325 330 335

Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala
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Pro Leu Lys Arg Lys Glu Thr Ser Asp Lys Thr Ser Lys Ala Ala Ala
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Asn Lys Lys Thr Lys Ala Gly Gly Lys Lys Lys
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gac aat gcg ccc aag gcg atg aag gag cag aag ttc gag agc tac ttc 159

Asp Asn Ala Pro Lys Ala Met Lys Glu Gln Lys Phe Glu Ser Tyr Phe

15 20 25

ggc gcg aaa atc gcc gtc gac gcc agc atg agc ata tac cag ttc ctg 207

Gly Arg Lys Ile Ala Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu

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att gta gtt gga agg aca ggc atg gaa act ctc aca aat gaa gct ggt 255

Ile Val Val Gly Arg Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly

45 50 55

gaa gtc act agt cat ttg caa gga atg ttc aac cgg aca ata aga tta 303

Glu Val Thr Ser His Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu

60 65 70 75

ctg gaa gcg gga atc aag cca gtt tat gtt ttt gat ggc aag cct cct 351

Leu Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro

80 85 90

gat atg aag aaa caa gag ctt gct aaa aga tac tca aaa aga gat gat 399

Asp Met Lys Lys Gln Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp

95 100 105

gca acc aaa gat ctg act gag gca gta gag gta gga gat aaa gat gcg 447

Ala Thr Lys Lys Asp Leu Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala

110 115 120

att gaa aaa ttg agc aag agg act gta aag gtc aca agg caa cac aac 495

Ile Glu Lys Leu Ser Lys Arg Thr Val Lys Val Thr Arg Gln His Asn

125 130 135

gaa gat tgt aaa cgg cta tta aga ctt atg ggg gtt cct gtt gta gag 543

Glu Asp Cys Lys Arg Leu Leu Arg Leu Met Gly Val Pro Val Val Glu

140 145 150 155

gca cct tct gaa gca gaa gca gaa tgt gca gcc ctt tgc ata aac gat 591

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Lys	Val	Phe	Ala	Val	Ala	Ser	Glu	Asp	Met	Asp	Ser	Leu	Thr	Phe	Gly		
			175					180					185				
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Ala	Pro	Arg	Phe	Leu	Arg	His	Leu	Met	Asp	Pro	Ser	Ser	Lys	Lys	Ile		
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cct	gtg	atg	gaa	ttt	gat	ggt	gcc	aag	ggt	ttg	gag	gag	ctt	gaa	ctc		735
Pro	Val	Met	Glu	Phe	Asp	Val	Ala	Lys	Val	Leu	Glu	Glu	Leu	Glu	Leu		
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Thr	Met	Asp	Gln	Phe	Ile	Asp	Leu	Cys	Ile	Leu	Cys	Gly	Cys	Asp	Tyr		
220					225					230					235		
tgt	gat	agc	atc	aaa	ggt	atc	ggg	ggg	caa	aca	gct	ctg	aaa	ctt	att		831
Cys	Asp	Ser	Ile	Lys	Gly	Ile	Gly	Gly	Gln	Thr	Ala	Leu	Lys	Leu	Ile		
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cgt	caa	cat	ggg	tcc	ata	gaa	agc	atc	ttg	gag	aat	ctt	aat	aaa	gac		879
Arg	Gln	His	Gly	Ser	Ile	Glu	Ser	Ile	Leu	Glu	Asn	Leu	Asn	Lys	Asp		
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Phe	Lys	Glu	Pro	Asn	Val	Thr	Leu	Asp	Ile	Pro	Glu	Leu	Lys	Trp	Thr		
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gca	cct	gat	gag	gag	ggt	ctc	ata	agt	ttc	ctg	gta	aaa	gat	aat	ggt		1023
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Phe	Asn	Glu	Asp	Arg	Arg	Lys	Lys	Ala	Ile	Glu	Lys	Ile	Lys	Ser	Ala		
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Lys	Asn	Lys	Ser	Ser	Gln	Gly	Arg	Leu	Glu	Ser	Phe	Phe	Lys	Pro	Thr		
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gcc	acc	aca	tca	gca	ccg	cta	aaa	cgg	aag	gag	act	tcg	gat	aaa	aca		1167
Ala	Thr	Thr	Ser	Ala	Pro	Leu	Lys	Arg	Lys	Glu	Thr	Ser	Asp	Lys	Thr		
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Ser	Lys	Ala	Ala	Ala	Asn	Lys	Lys	Thr	Lys	Ala	Gly	Gly	Lys	Lys	Lys		
			365			370					375						
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 35 40 45
 Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly Glu Val Thr Ser His
 50 55 60
 Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu Leu Glu Ala Gly Ile
 65 70 75 80
 Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Asp Met Lys Lys Gln
 85 90 95
 Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp Ala Thr Lys Asp Leu
 100 105 110
 Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala Ile Glu Lys Leu Ser
 115 120 125
 Lys Arg Thr Val Lys Val Thr Arg Gln His Asn Glu Asp Cys Lys Arg
 130 135 140
 Leu Leu Arg Leu Met Gly Val Pro Val Val Glu Ala Pro Ser Glu Ala
 145 150 155 160
 Glu Ala Glu Cys Ala Ala Leu Cys Ile Asn Asp Lys Val Phe Ala Val
 165 170 175
 Ala Ser Glu Asp Met Asp Ser Leu Thr Phe Gly Ala Pro Arg Phe Leu
 180 185 190
 Arg His Leu Met Asp Pro Ser Ser Lys Lys Ile Pro Val Met Glu Phe
 195 200 205
 Asp Val Ala Lys Val Leu Glu Glu Leu Glu Thr Met Asp Gln Phe
 210 215 220
 Ile Asp Leu Cys Ile Leu Cys Gly Cys Asp Tyr Cys Asp Ser Ile Lys
 225 230 235 240
 Gly Ile Gly Gly Gln Thr Ala Leu Lys Leu Ile Arg Gln His Gly Ser
 245 250 255
 Ile Glu Ser Ile Leu Glu Asn Leu Asn Lys Asp Arg Tyr Gln Ile Pro
 260 265 270
 Glu Asp Trp Pro Tyr Gln Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn
 275 280 285
 Val Thr Leu Asp Ile Pro Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu
 290 295 300
 Gly Leu Ile Ser Phe Leu Val Lys Asp Asn Gly Phe Asn Glu Asp Arg
 305 310 315 320
 Val Arg Lys Ala Ile Glu Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser
 325 330 335
 Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala
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aat ctt aat aaa gac aga tat caa att cct gag gac tgg cct tac caa Asn Leu Asn Lys Asp Arg Tyr Gln Ile Pro Glu Asp Trp Pro Tyr Gln 265 270 275	870
gaa gct cga cgc ttg ttc aag gag cct aat gtc aca ttg gat att cct Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro 280 285 290	918
gag cta aaa tgg act gca cct gat gag gag ggt ctc ata agt ttc ctg Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu Gly Leu Ile Ser Phe Leu 295 300 305 310	966
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 35 40 45
 Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly Glu Val Thr Ser His
 50 55 60

Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu Leu Glu Ala Gly Ile
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 Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Asp Met Lys Lys Gln
 85 90 95
 Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Ala Thr Lys Asp Leu
 100 105 110
 Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala Ile Glu Lys Leu Ser
 115 120 125
 Lys Arg Thr Val Lys Val Thr Arg Gln His Asn Glu Asp Cys Lys Arg
 130 135 140
 Leu Leu Arg Leu Met Gly Val Pro Val Val Glu Ala Pro Ser Glu Ala
 145 150 155 160
 Glu Ala Glu Cys Ala Ala Leu Cys Ile Asn Asp Lys Val Phe Ala Val
 165 170 175
 Ala Ser Glu Asp Met Asp Ser Leu Thr Phe Gly Ala Pro Arg Phe Leu
 180 185 190
 Arg His Leu Met Asp Pro Ser Ser Lys Lys Ile Pro Val Met Glu Phe
 195 200 205
 Asp Val Ala Lys Val Leu Glu Glu Leu Glu Thr Met Asp Gln Phe
 210 215 220
 Ile Asp Leu Cys Ile Leu Cys Gly Cys Asp Tyr Cys Asp Ser Ile Lys
 225 230 235 240
 Gly Ile Gly Gly Gln Thr Ala Leu Lys Leu Ile Arg Gln His Gly Ser
 245 250 255
 Ile Glu Ser Ile Leu Glu Asn Leu Asn Lys Asp Arg Tyr Gln Ile Pro
 260 265 270
 Glu Asp Trp Pro Tyr Gln Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn
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 Val Thr Leu Asp Ile Pro Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu
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 Gly Leu Ile Ser Phe Leu Val Lys Asp Asn Gly Phe Asn Glu Asp Arg
 305 310 315 320
 Val Thr Lys Ala Ile Glu Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser
 325 330 335
 Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala
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 Met Gly Ile Lys Gly Leu
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 acg aaa ctg ctg gcg gac aat gcg ccc aag gcg atg aag gag cag aag 162
 Thr Lys Leu Leu Ala Asp Asn Ala Pro Lys Ala Met Lys Glu Gln Lys
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 ttc gag agc tac ttc ggc cgc aaa atc gcc gtc gag gcc agc atg agc 210

Phe	Glu	Ser	Tyr	Phe	Gly	Arg	Lys	Ile	Ala	Val	Asp	Ala	Ser	Met	Ser	
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Ile	Tyr	Gln	Phe	Leu	Ile	Val	Val	Gly	Arg	Thr	Gly	Met	Glu	Thr	Leu	
	40					45					50					
aca	aat	gaa	gct	ggt	gaa	gtc	act	agt	cat	ttg	caa	gga	atg	ttc	aac	306
Thr	Asn	Glu	Ala	Gly	Glu	Val	Thr	Ser	His		Leu	Gln	Gly	Met	Phe	
	55				60					65					70	
cgg	aca	ata	aga	tta	ctg	gaa	gcg	gga	atc	aag	cca	gtt	tat	gtt	ttt	354
Arg	Thr	Ile	Arg	Leu	Leu	Glu	Ala	Gly	Ile	Lys	Pro	Val	Tyr	Val	Phe	
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gat	ggc	aag	cct	cct	gat	atg	aag	aaa	caa	gaa	ctt	gct	aaa	aga	tac	402
Asp	Gly	Lys	Pro	Pro	Asp	Met	Lys	Lys	Gln	Glu	Leu	Ala	Lys	Arg	Tyr	
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tca	aaa	aga	gat	gat	gca	acc	aaa	gat	ctg	act	gag	gca	gta	gag	gta	450
Ser	Lys	Arg	Asp	Asp	Ala	Thr	Lys	Asp	Leu	Thr	Glu	Ala	Val	Glu	Val	
	105						110					115				
gga	gat	aaa	gat	gcg	att	gaa	aaa	ttg	agc	aag	agg	act	gta	aag	gtc	498
Gly	Asp	Lys	Asp	Ala	Ile	Glu	Lys	Leu	Ser	Lys	Arg	Thr	Val	Lys	Val	
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aca	agg	caa	cac	aac	gaa	gat	tgt	aaa	cga	cta	tta	aga	ctt	atg	ggg	546
Thr	Arg	Gln	His	Asn	Glu	Asp	Cys	Lys	Arg	Leu	Leu	Arg	Leu	Met	Gly	
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Val	Pro	Val	Val	Glu	Ala	Pro	Ser	Glu	Ala	Glu	Ala	Glu	Cys	Ala	Ala	
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ctt	tgc	ata	aac	gat	aag	gtg	ttc	gct	gtt	gct	tca	gaa	gat	aag	gac	642
Leu	Cys	Ile	Asn	Asp	Lys	Val	Phe	Ala	Val	Ala	Ser	Glu	Asp	Lys	Asp	
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tcc	ctt	act	ttt	ggg	gct	cca	cgg	ttc	ctt	cgt	cat	tta	atg	gat	cca	690
Ser	Leu	Thr	Phe	Gly	Ala	Pro	Arg	Phe	Leu	Arg	His	Leu	Met	Asp	Pro	
	185						190					195				
agt	tcc	aag	aaa	ata	cct	gtg	atg	gaa	ttt	gat	gtt	gcc	aag	gtt	ttg	738
Ser	Ser	Lys	Lys	Ile	Pro	Val	Met	Glu	Phe	Asp	Val	Ala	Lys	Val	Leu	
	200					205					210					
gag	gag	ctt	gaa	ctc	acc	atg	gac	cag	ttc	att	gat	ttg	tgc	atc	ctg	786
Glu	Glu	Leu	Glu	Leu	Thr	Met	Asp	Gln	Phe	Ile	Asp	Leu	Cys	Ile	Leu	
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tgt	gga	tgt	gac	tat	tgt	gat	agc	atc	aaa	ggg	atc	ggg	ggg	caa	aca	834
Cys	Gly	Cys	Asp	Tyr	Cys	Asp	Ser	Ile	Lys	Gly	Ile	Gly	Gly	Gln	Thr	
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gct	ctg	aaa	ctt	att	cgt	caa	cat	ggg	tcc	ata	gaa	agc	atc	ttg	gag	882
Ala	Leu	Lys	Leu	Ile	Arg	Gln	His	Gly	Ser	Ile	Glu	Ser	Ile	Leu	Glu	
			250					255					260			
aat	ctt	aat	aaa	gac	aga	tat	caa	att	cct	gag	gac	tgg	cct	tac	caa	930
Asn	Leu	Asn	Lys	Asp	Arg	Tyr	Gln	Ile	Pro	Glu	Asp	Trp	Pro	Tyr	Gln	
	265						270					275				

gaa gct cga cgc ttg ttc aag gag cct aat gtc act ttg gat att cct	978
Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro	
280 285 290	
gag cta aaa tgg act gca cct gat gag gag ggt ctc ata agt ttc ctg	1026
Glu Leu Lys Trp Thr Ala Pro Asp Glu Gly Leu Ile Ser Phe Leu	
295 300 305 310	
gta aaa gat aat ggt ttc aat gaa gat cgg gtg aca aag gcc ata gag	1074
Val Lys Asp Asn Gly Phe Asn Glu Asp Arg Val Thr Lys Ala Ile Glu	
315 320 325	
aag atc aaa tct gcc aag aat aaa tcg tcg caa gga aga ctc gag tcc	1122
Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser	
330 335 340	
ttt ttc aag cca act gcc acc aca tca gca cgg cta aaa cgg aag gag	1170
Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala Pro Leu Lys Arg Lys Glu	
345 350 355	
act tcg gat aaa aca agc aag gca gct gcg aac aag aaa aca aag gct	1218
Thr Ser Asp Lys Thr Ser Lys Ala Ala Asn Lys Lys Thr Lys Ala	
360 365 370	
ggt gga aag aag aaa taatcttggg tgcttgatgt acaactacga ctacgaaagc	1273
Gly Gly Lys Lys Lys	
375	
agcgggtggca tgatcacttc gcctagatta ttttaactccc tggttttaact cagacotttg	1333
gtgaaagttt gcccatgttt caagctgggg taagtttagtt gtggttggaag agattgggtg	1393
accaagtaac aaaacttctc gctgtttttt acttcttctgc ctttgaagta tgtatgcacg	1453
taaaaaaaaa aaaaaaaaaa aaaaa	1478
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Ala Met Lys Glu Gln Lys Phe Glu Ser Tyr Phe Gly Arg Lys Ile Ala	
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Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Val Val Gly Arg	
35 40 45	
Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly Glu Val Thr Ser His	
50 55 60	
Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu Glu Ala Gly Ile	
65 70 75 80	
Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Asp Met Lys Lys Gln	
85 90 95	
Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp Ala Thr Lys Asp Leu	
100 105 110	
Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala Ile Glu Lys Leu Ser	
115 120 125	
Lys Arg Thr Val Lys Val Thr Arg Gln His Asn Glu Asp Cys Lys Arg	
130 135 140	
Leu Leu Arg Leu Met Gly Val Pro Val Val Glu Ala Pro Ser Glu Ala	
145 150 155 160	

Glu Ala Glu Cys Ala Ala Leu Cys Ile Asn Asp Lys Val Phe Ala Val
 165 170 175
 Ala Ser Glu Asp Lys Asp Ser Leu Thr Phe Gly Ala Pro Arg Phe Leu
 180 185 190
 Arg His Leu Met Asp Pro Ser Ser Lys Ile Pro Val Met Glu Phe
 195 200 205
 Asp Val Ala Lys Val Leu Glu Glu Leu Thr Met Asp Gln Phe
 210 215 220
 Ile Asp Leu Cys Ile Leu Cys Gly Cys Asp Tyr Cys Asp Ser Ile Lys
 225 230 235 240
 Gly Ile Gly Gly Gln Thr Ala Leu Lys Leu Ile Arg Gln His Gly Ser
 245 250 255
 Ile Glu Ser Ile Leu Glu Asn Leu Asn Lys Asp Arg Tyr Gln Ile Pro
 260 265 270
 Glu Asp Trp Pro Tyr Gln Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn
 275 280 285
 Val Thr Leu Asp Ile Pro Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu
 290 295 300
 Gly Leu Ile Ser Phe Leu Val Lys Asp Asn Gly Phe Asn Glu Asp Arg
 305 310 315 320
 Val Thr Lys Ala Ile Glu Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser
 325 330 335
 Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala
 340 345 350
 Pro Leu Lys Arg Lys Glu Thr Ser Asp Lys Thr Ser Lys Ala Ala Ala
 355 360 365
 Asn Lys Lys Thr Lys Ala Gly Gly Lys Lys Lys
 370 375

<210> 9

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide based upon an adaptor
 used for cDNA library construction and poly(dT) to
 remove clones which have a poly(A) tail but no
 cDNA insert.

<400> 9

tcgacccacg cgctccgaaaa aaaaaaaaaa aaaaaa
 36

<210> 10

<211> 380

<212> PRT

<213> Homo sapiens

<400> 10

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 Ala Ile Arg Glu Asn Asp Ile Lys Ser Tyr Phe Gly Arg Lys Val Ala
 20 25 30
 Ile Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Ala Val Arg Gln
 35 40 45
 Gly Gly Asp Val Leu Gln Asn Glu Glu Gly Glu Thr Thr Ser His Leu
 50 55 60
 Met Gly Met Phe Tyr Arg Thr Ile Arg Met Met Glu Asn Gly Ile Lys
 65 70 75 80

Pro	Val	Tyr	Val	Phe	Asp	Gly	Lys	Pro	Pro	Gln	Leu	Lys	Ser	Gly	Glu
				85					90					95	
Leu	Ala	Lys	Arg	Ser	Glu	Arg	Arg	Ala	Glu	Ala	Glu	Lys	Gln	Leu	Gln
			100					105					110		
Gln	Ala	Gln	Ala	Ala	Gly	Ala	Glu	Gln	Glu	Val	Glu	Lys	Phe	Thr	Lys
			115				120						125		
Arg	Leu	Val	Lys	Val	Thr	Lys	Gln	His	Asn	Asp	Glu	Cys	Lys	His	Leu
	130					135					140				
Leu	Ser	Leu	Met	Gly	Ile	Pro	Tyr	Leu	Asp	Ala	Pro	Ser	Glu	Ala	Glu
	145				150					155					160
Ala	Ser	Cys	Ala	Ala	Leu	Val	Lys	Ala	Gly	Lys	Val	Tyr	Ala	Ala	Ala
			165						170					175	
Thr	Glu	Asp	Met	Asp	Cys	Leu	Thr	Phe	Gly	Ser	Pro	Val	Leu	Met	Arg
			180						185				190		
His	Leu	Thr	Ala	Ser	Glu	Ala	Lys	Lys	Leu	Pro	Ile	Gln	Glu	Phe	His
		195					200					205			
Leu	Ser	Arg	Ile	Leu	Gln	Glu	Leu	Gly	Leu	Asn	Gln	Glu	Gln	Phe	Val
		210				215					220				
Asp	Leu	Cys	Ile	Leu	Leu	Gly	Ser	Asp	Tyr	Cys	Glu	Ser	Ile	Arg	Gly
	225				230					235					240
Ile	Gly	Pro	Lys	Arg	Ala	Val	Asp	Leu	Ile	Gln	Lys	His	Lys	Ser	Ile
			245						250					255	
Glu	Glu	Ile	Val	Arg	Arg	Leu	Asp	Pro	Asn	Lys	Tyr	Pro	Val	Pro	Glu
			260					265					270		
Asn	Trp	Leu	His	Lys	Glu	Ala	His	Gln	Leu	Phe	Leu	Glu	Pro	Glu	Val
		275					280					285			
Leu	Asp	Pro	Glu	Ser	Val	Glu	Leu	Lys	Trp	Ser	Glu	Pro	Asn	Glu	Glu
		290				295					300				
Glu	Leu	Ile	Lys	Phe	Met	Cys	Gly	Glu	Lys	Gln	Phe	Ser	Glu	Glu	Arg
	305				310					315					320
Ile	Arg	Ser	Gly	Val	Lys	Arg	Leu	Ser	Lys	Ser	Arg	Gln	Gly	Ser	Thr
			325						330					335	
Gln	Gly	Arg	Leu	Asp	Asp	Phe	Phe	Lys	Val	Thr	Gly	Ser	Leu	Ser	Ser
			340					345					350		
Ala	Lys	Arg	Lys	Glu	Pro	Glu	Pro	Lys	Gly	Ser	Thr	Lys	Lys	Lys	Ala
		355					360						365		
Lys	Thr	Gly	Ala	Ala	Gly	Lys	Phe	Lys	Arg	Gly	Lys				
	370					375					380				